

To: (10)(2e) <(10)(2e)@rivm.nl>
From: (10)(2e)
Sent: Tue 12/1/2020 7:51:42 AM
Subject: FW: update model-based inference
Received: Tue 12/1/2020 7:51:44 AM

From: (10)(2e) <(10)(2e)@rivm.nl>
Sent: woensdag 22 juli 2020 15:54
To: (10)(2e) <(10)(2e)@rivm.nl>; (10)(2e) <(10)(2e)@rivm.nl>
Subject: FW: update model-based inference

Hallo (10)(2e),

Ter info, onderstaande heb ik net naar (10)(2e) gestuurd zodat zij realistische parameterwaardes kan gebruiken in haar scenariostudies. (10)(2e) weten dat ik daar niet aan kan bijdragen.

Ik hoop wel dat ik tzt met oa (10)(2e) iets kan schrijven over het schatten van parameters met een nieuwe methode (zie ook hieronder). Daar had ik het gisteren kort met jullie over gehad. Graag hoor ik wat jullie daarvan vinden.

(10)(2e)

From: (10)(2e)
Sent: woensdag 22 juli 2020 15:35
To: (10)(2e) <(10)(2e)@umcutrecht.nl>; (10)(2e) <(10)(2e)@gmail.com>
Cc: (10)(2e) <(10)(2e)@umcutrecht.nl>; (10)(2e) <(10)(2e)@umcutrecht.nl>
Subject: update model-based inference

Dear all,

Attached and below you find a recent update of the code for model-based inference using actual hospitalization data and synthetic serological data (n=3,000 in the first week of April, 10 groups of 300 with 8 infections in each group). The synthetic serological data are important to ensure that the age-specific attack rates are reasonable (2-3% late March). This can at any moment be updated with actual serological data.

By request of ao (10)(2e) I have today

- 1) lumped the age groups 0-4, 5-9, and 10-19 years as well as the age groups 20-29, 30-39, 40-49 years wrt hospitalization rates,
- 2) included a smooth logistic transition from the pre-lockdown contact matrix to the lockdown contact matrix,
- 3) estimated the parameters x_0 and k of the transition function as well as a reduction factor (ζ) for the additional reduction in transmission during the lockdown, and
- 4) included (by example) the possibility of estimation of the age-dependent fractions that were already immune (or less infectious, is also straightforward).

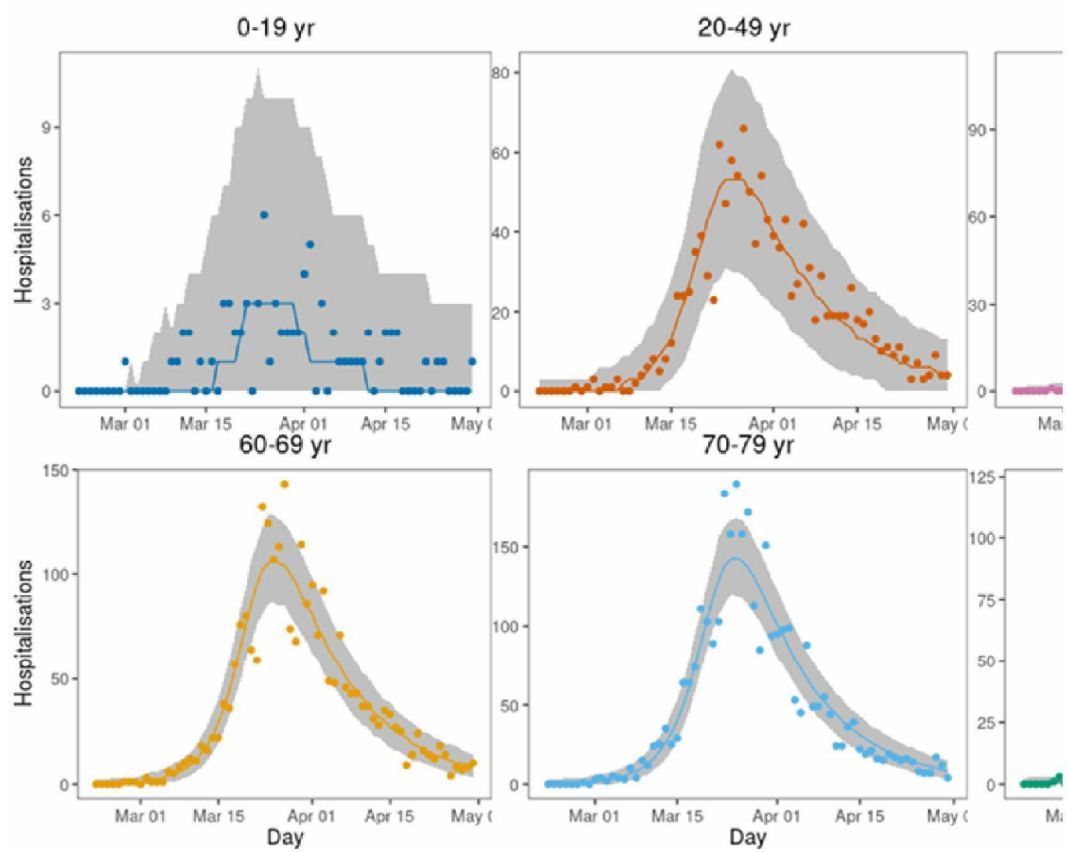
Below you also find some plots and statistics. Let me know if you have questions or remarks.

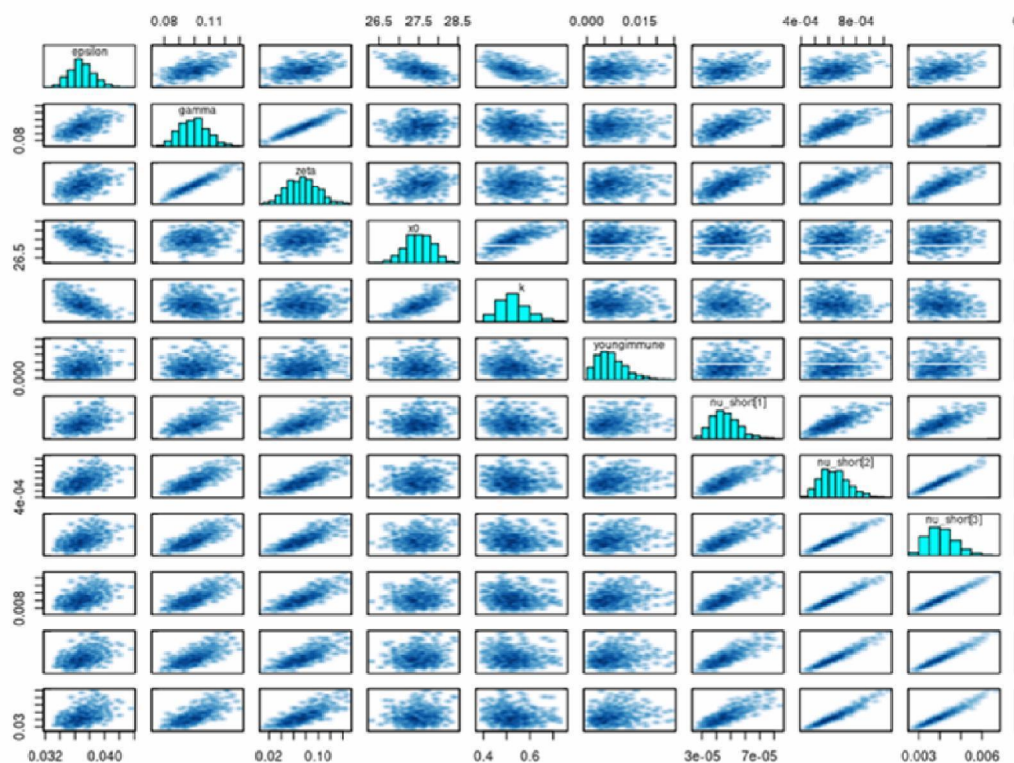
As you know I may not be able to publish with you on exit/de-escalation scenario studies, so I will now leave any further refinements as well as subsequent model scenario analyses to (10)(2e). Good luck with it!

I do hope to be able to write something on estimation of transmission parameters, attack rates, and age-dependent hospitalisation probabilities with generalized profiling (along the lines of earlier influenza/rsv work; see e.g.

(10)(2e). For this I think we will ultimately need actual serological data. I was hoping that (10)(2e) <(10)(2e)> could reformulate the current model to GP and produce some figures (still with the synthetic serodata). Is that ok with you, (10)(2e)? After that, I will write a draft (shouldn't take more than a couple of days) and share this first with (10)(2e) <(10)(2e)> and (10)(2e) <(10)(2e)> and thereafter with others (including ao (10)(2e) <(10)(2e)>) to see who could/would be willing and deserving to contribute.

Best,
 (10)(2e)





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Inference for Stan model: corona_21072020.
10 chains, each with iter=2000; warmup=1000; thin=10;
post-warmup draws per chain=100, total post-warmup draws=1000.

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	mean	se_mean	sd	2.5%	25%	50%	75%	97.5%	n_eff
Rhat									
epsilon 0.998110	0.036932	0.000054	0.001651	0.033973	0.035834	0.036832	0.037955	0.040519	919
gamma 0.998408	0.099491	0.000308	0.009248	0.082982	0.092866	0.099397	0.105437	0.119651	904
zeta 1.000717	0.074417	0.000810	0.024907	0.029401	0.056184	0.073972	0.091235	0.125613	945
x0 0.998025	27.500285	0.010659	0.346750	26.801352	27.272322	27.496246	27.748264	28.159879	1058
k 0.994094	0.529263	0.002107	0.063514	0.420141	0.484733	0.522537	0.568994	0.674388	908
youngimmune 1.000339	0.007151	0.000138	0.004370	0.001099	0.003931	0.006457	0.009478	0.017732	1006
nu_short[1] 0.998242	0.000046	0.000000	0.000010	0.000031	0.000039	0.000045	0.000052	0.000069	1060
nu_short[2] 1.000751	0.000644	0.000003	0.000105	0.000472	0.000566	0.000637	0.000707	0.000869	1005
nu_short[3] 1.000789	0.004071	0.000022	0.000679	0.002989	0.003564	0.004009	0.004486	0.005641	991

nu_short[4]	0.010430	0.000056	0.001758	0.007662	0.009121	0.010278	0.011442	0.014384	992
1.001132									
nu_short[5]	0.027358	0.000161	0.005103	0.019341	0.023644	0.026808	0.030218	0.039103	1003
1.000078									
nu_short[6]	0.044036	0.000283	0.009041	0.030369	0.037444	0.042654	0.049252	0.065640	1019
0.999616									
inoculum	0.000031	0.000000	0.000007	0.000019	0.000026	0.000030	0.000035	0.000045	919
1.000869									
p_short[1]	0.000464	0.000002	0.000074	0.000333	0.000414	0.000456	0.000513	0.000629	1070
0.998066									
p_short[2]	0.006411	0.000021	0.000662	0.005246	0.005924	0.006384	0.006844	0.007816	1009
1.000936									
p_short[3]	0.039162	0.000130	0.004045	0.031956	0.036275	0.038776	0.041653	0.047602	965
1.001540									
p_short[4]	0.094506	0.000307	0.009582	0.077494	0.088031	0.093623	0.100849	0.115218	976
1.000875									
p_short[5]	0.214390	0.000699	0.021959	0.175166	0.199403	0.212917	0.227400	0.261822	987
1.000535									
p_short[6]	0.304343	0.000962	0.030799	0.249242	0.282099	0.302270	0.324068	0.371028	1026
0.999536									

Samples were drawn using NUTS(diag_e) at Wed Jul 22 13:30:32 2020.
 For each parameter, n_eff is a crude measure of effective sample size,
 and Rhat is the potential scale reduction factor on split chains (at
 convergence, Rhat=1).

 (10)(2e)
 Centre for Infectious Disease Control
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